CLAIMS

WHAT IS CLAIMED IS:

1. An oligonucleotide consisting of a nucleic acid with a sequence selected from the group consisting of: SEQ ID NOS: 1-12 and 15-24 and complements thereof.

2. An oligonucleotide comprising a nucleic acid with a sequence selected from the group consisting of: SEQ ID NOS: 1-12 and 15-24 and complements thereof, which oligonucleotide has 100 or fewer nucleotides.

3. The oligonucleotide of claim 2, wherein the oligonucleotide comprises a probe nucleic acid or a primer nucleic acid.

4. The oligonucleotide of claim 2, wherein the oligonucleotide comprises at least one modified nucleotide.

5. The oligonucleotide of claim 2, wherein the oligonucleotide comprises at least one label and/or at least one quencher moiety.

6. The oligonucleotide of claim 2, wherein the oligonucleotide has 40 or fewer nucleotides.

7. An oligonucleotide comprising a nucleic acid having at least 90% sequence identity to one of SEQ ID NOS: 1-12 and 15-24 or a complement thereof, which oligonucleotide has 100 or fewer nucleotides.

8. The oligonucleotide of claim 7, wherein the nucleic acid has at least 95% sequence identity to one of SEQ ID NOS: 1-12 and 15-24 or the complement thereof.

9. The oligonucleotide of claim 7, wherein the oligonucleotide comprises at least one modified nucleotide.

10. The oligonucleotide of claim 7, wherein the oligonucleotide comprises at least one label and/or at least one quencher moiety.

11. The oligonucleotide of claim 7, wherein the oligonucleotide has 40 or fewer nucleotides.

12. The oligonucleotide of claim 7, wherein the oligonucleotide comprises at least one conservatively modified variation.

13. A method of detecting a severe acute respiratory syndrome coronavirus in a sample, the method comprising:

(a) contacting nucleic acids from the sample with at least one primer nucleic acid comprising at least one nucleic acid selected from the group consisting of: SEQ ID NOS: 1-12 and 15-24 and complements thereof in at least one nucleic acid amplification reaction; and,

(b) detecting the nucleic acids and/or one or more amplicons thereof from the nucleic acid amplification reaction during or after (a), thereby detecting the severe acute respiratory syndrome coronavirus in the sample.

14. The method of claim 13, wherein at least one of the primer nucleic acids comprises a modified primer nucleic acid.

15. The method of claim 13, wherein at least one of the amplicons is about 440 nucleotides in length.

16. The method of claim 13, wherein at least one round of the nucleic acid amplification reaction is performed using primer nucleic acids comprising sequences selected from SEQ ID NOS: 11 or 22 and SEQ ID NOS: 12 or 20.

17. The method of claim 13, wherein at least one round of the nucleic acid amplification reaction is performed using primer nucleic acids comprising sequences selected from SEQ ID NOS: 15 or 18 and SEQ ID NOS: 16 or 19.

18. The method of claim 13, wherein the nucleic acid amplification reaction comprises a nested polymerase chain reaction.

19. The method of claim 13, wherein at least one of the primer nucleic acids comprises at least one label.

20. The method of claim 19, wherein (b) comprises detecting a detectable signal produced by the label, or amplifying a detectable signal produced by the label to produce an amplified signal and detecting the amplified signal.

21. The method of claim 13, wherein (b) comprises monitoring binding between the amplicons and at least one oligonucleotide having a sequence selected from the group consisting of: SEQ ID NOS: 1-12 and 15-24, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID

NOS: 1-12 and 15-24, and complements of SEQ ID NOS: 1-12 and 15-24 and the variant.

22. The method of claim 21, wherein the oligonucleotide comprises at least one label and/or at least one quencher moiety.

23. The method of claim 22, wherein the oligonucleotide comprises a 5'-nuclease probe having a sequence selected from SEQ ID NO: 27 or SEQ ID NO: 28.

24. A method of determining a presence of a severe acute respiratory syndrome coronavirus in a sample, the method comprising:

(a) contacting nucleic acids and/or amplicons thereof from the sample with one or more oligonucleotides that comprise at least one nucleic acid with a sequence selected from the group consisting of: SEQ ID NOS: 1-12 and 15-24, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 1-12 and 15-24, and complements of SEQ ID NOS: 1-12 and 15-24 and the variant; and,

(b) monitoring binding between the nucleic acids and/or amplicons thereof, and the oligonucleotides, wherein detectable binding between the nucleic acids and/or amplicons thereof, and the oligonucleotides, determines the presence of the severe acute respiratory syndrome coronavirus in the sample.

25. The method of claim 24, wherein (a) comprises contacting the nucleic acids and/or amplicons thereof with the oligonucleotides in solution at a temperature of at least 42°C for at least 15 minutes, wherein a total weight of the solution comprises about 50% formalin and comprises heparin at a concentration of about 1 mg/ml.

26. The method of claim 24, comprising repeating (a) and (b) at least once using at least one additional sample and comparing the binding between the nucleic acids and/or amplicons thereof, and the oligonucleotides, of (b) with at least one repeated (b).

27. The method of claim 24, wherein at least one segment of the nucleic acids is amplified prior to or during (a) using at least one nucleic acid amplification technique to produce the amplicons and (b) comprises monitoring the binding between the nucleic acids and/or amplicons thereof, and the oligonucleotides, during or after amplification.

28. A composition comprising a sample derived from a subject and at least one oligonucleotide that comprises a nucleic acid with a sequence selected from the group consisting of: SEQ ID NOS: 1-12 and 15-24, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 1-12 and 15-24, and complements of SEQ ID NOS: 1-12 and 15-24 and the variant, which oligonucleotide consists of 100 or fewer nucleotides.

29. A kit, comprising:

(a) at least one oligonucleotide that comprises a nucleic acid with a sequence selected from the group consisting of: SEQ ID NOS: 1-12 and 15-24, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 1-12 and 15-24, and complements of SEQ ID NOS: 1-12 and 15-24 and the variant, which oligonucleotide consists of 100 or fewer nucleotides; and one or more of:

(b) instructions for determining a presence of a severe acute respiratory syndrome coronavirus in a sample by monitoring binding between nucleic acids and/or amplicons thereof from the sample and the oligonucleotide, wherein the presence of the severe acute respiratory syndrome coronavirus in the sample is unknown or unsubstantiated; or,

(c) at least one container for packaging at least the oligonucleotide.

30. The kit of claim 29, further comprising at least one enzyme.

31. A system for detecting a severe acute respiratory syndrome coronavirus in a sample, comprising:

(a) at least one oligonucleotide that comprises a nucleic acid with a sequence selected from the group consisting of: SEQ ID NOS: 1-12 and 15-24, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 1-12 and 15-24, and complements of SEQ ID NOS: 1-12 and 15-24 and the variant, which oligonucleotide consists of 100 or fewer nucleotides;

(b) at least one detector that detects binding between nucleic acids and/or amplicons thereof from the sample and the oligonucleotide; and,

(c) at least one controller operably connected to the detector, which controller comprises one or more instructions sets that correlate the binding detected by the detector with a presence of the severe acute respiratory syndrome coronavirus in the sample.

32. A system, comprising:

(a) computer or computer readable medium comprising a data set that comprises a plurality of character strings that correspond to a plurality of sequences that correspond to one or more of: SEQ ID NOS: 1-12 and 15-24, a substantially identical variant thereof wherein the variant has at least 90% sequence identity to one of SEQ ID NOS: 1-12 and 15-24, and complements of SEQ ID NOS: 1-12 and 15-24 and the variant; and,

(b) an automatic synthesizer coupled to an output of the computer or computer readable medium, which automatic synthesizer accepts instructions from the computer or computer readable medium, which instructions direct synthesis of one or more nucleic acids that correspond to one or more character strings in the data set.